

L3 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1974:504464 CAPLUS
DN 81:104464
TI Organic transition states. II. Methylenecyclopropane rearrangement.
Two-step diradical pathway with a secondary minimum
AU Hehre, W. J.; Salem, L.; Willcott, M. R.
CS Lab. Chim. Theor., Univ. Paris-Sud, Orsay, Fr.
SO Journal of the American Chemical Society (1974),
96(13), 4328-30
CODEN: JACSAT; ISSN: 0002-7863
DT Journal
LA English

L6 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN
AN 1974:505883 CAPLUS
DN 81:105883
TI Structure of coformycin, an unusual nucleoside of microbial origin
AU Nakamura, Hikaru; Koyama, Gunji; Iitaka, Yoichi; Ohno, Masaji;
Yagisawa, Naomasa; Kondo, Shinichi; Maeda, Kenji; Umezawa, Hamao
CS Fac, Pharm. Sci., Univ. Tokyo, Tokyo, Japan
SO Journal of the American Chemical Society (1974),
96(13) 4327-8
CODEN: JACSAT; ISSN: 0002-7863
DT Journal
LA English
OS CASREACT 81:105883

SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 10, 2004, 16:42:31 ; Search time 115 Seconds
(without alignments)
2330.181 Million cell updates/sec

Title: US-10-022-366A-2
Perfect score: 3949
Sequence: 1 MPLFKLPAEGKELDDAMGSF.....RYETWCYELNLIAEGLKSTE 747
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3949	100.0	747	5	ABG70650 <i>EP 12/5587</i>	Abg70650 Rabbit ad
2	3728	94.4	747	7	ADJ68732 <i>WO 03/87768</i>	Adj68732 Human hea
3	3728	94.4	747	8	ADM32868 <i>WO 04/24880</i>	Adm32868 Protein s - human
4	3728	94.4	747	8	ADQ18475 <i>WO 04/48938</i>	Adq18475 Human sof "
5	3728	94.4	747	8	ADP87621 <i>WO 04/56961</i>	Adp87621 Human NOV
6	3728	94.4	748	8	ADP87625 <i>WO 04/56961</i>	Adp87625 Human NOV
7	3728	94.4	751	8	ADP87623 "	Adp87623 Human NOV
8	3621.5	91.7	1813	4	ABG02232 <i>WO 01/075067</i>	Abg02232 Novel hum
9	3607	91.3	747	8	ADP87685	Adp87685 Rat AMP-a
10	3302	83.6	654	8	ADP87635	Adp87635 Human NOV
11	3302	83.6	654	8	ADP87627	Adp87627 Human NOV
12	3302	83.6	660	8	ADP87637	Adp87637 Human NOV
13	3302	83.6	660	8	ADP87631	Adp87631 Human NOV
14	3298	83.5	661	8	ADP87629	Adp87629 Human NOV
15	3298	83.5	661	8	ADP87633	Adp87633 Human NOV
16	2407.5	61.0	776	8	ADM32870	Adm32870 Protein s
17	2401	60.8	801	7	ADB79947	Adb79947 Rat AMP d
18	1917	48.5	438	7	ADM05430	Adm05430 Human pro

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OM protein - protein search, using sw model

Run on: December 10, 2004, 16:42:31 ; Search time 1444 Seconds
(without alignments)
184.773 Million cell updates/sec

Title: US-10-022-366A-2
Perfect score: 3949
Sequence: 1 MPLFKLPAEGKELDDAMGSF.....RYETWCYELNLIAEGLKSTE 747

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query

No.	Score	Match	Length	DB	ID	Description
1	3949	100.0	747	15	US-10-022-366A-2	Sequence 2, Appli
2	3728	94.4	747	16	US-10-408-765A-538	Sequence 538, App
3	3613	91.5	752	16	US-10-322-281-772	Sequence 772, App
4	3511	88.9	732	16	US-10-322-281-769	Sequence 769, App
5	2401	60.8	801	14	US-10-205-219-187	Sequence 187, App
6	1917	48.5	438	15	US-10-108-260A-4115	Sequence 4115, Ap
7	1568	39.7	813	17	US-10-425-115-200019	Sequence 200019,
8	1490.5	37.7	544	16	US-10-437-963-171334	Sequence 171334,
9	1438	36.4	557	15	US-10-424-599-188513	Sequence 188513,
10	1096	27.8	577	17	US-10-425-115-328131	Sequence 328131,
11	1033.5	26.2	345	15	US-10-424-599-164796	Sequence 164796,
12	866.5	21.9	446	14	US-10-012-140-19	Sequence 19, Appl
13	710.5	18.0	268	17	US-10-425-115-328153	Sequence 328153,
14	615.5	15.6	219	16	US-10-767-701-35150	Sequence 35150, A
15	606.5	15.4	540	16	US-10-437-963-125822	Sequence 125822,
16	597	15.1	211	16	US-10-767-701-59704	Sequence 59704, A
17	549.5	13.9	308	15	US-10-424-599-276788	Sequence 276788,
18	416.5	10.5	145	16	US-10-437-963-140327	Sequence 140327,
19	348.5	8.8	241	16	US-10-767-701-34805	Sequence 34805, A
20	342	8.7	115	17	US-10-425-115-295726	Sequence 295726,
21	335	8.5	160	14	US-10-106-698-5825	Sequence 5825, Ap
22	324	8.2	65	9	US-09-864-761-42950	Sequence 42950, A
23	305	7.7	108	16	US-10-767-701-39882	Sequence 39882, A
24	291	7.4	106	16	US-10-767-701-41443	Sequence 41443, A
25	203	5.1	86	15	US-10-424-599-188512	Sequence 188512,
26	199	5.0	114	15	US-10-424-599-190598	Sequence 190598,
27	155	3.9	908	15	US-10-282-122A-47185	Sequence 47185, A
28	153.5	3.9	151	17	US-10-425-115-295117	Sequence 295117,
29	149	3.8	115	17	US-10-425-115-316899	Sequence 316899,
30	140	3.5	1116	14	US-10-369-493-2069	Sequence 2069, Ap
31	139	3.5	1102	14	US-10-369-493-1074	Sequence 1074, Ap
32	136.5	3.5	966	9	US-09-978-698-2	Sequence 2, Appli
33	135	3.4	968	14	US-10-342-224-14	Sequence 14, Appl
34	132	3.3	358	14	US-10-156-761-10132	Sequence 10132, A
35	130.5	3.3	1001	15	US-10-607-631-10	Sequence 10, Appl
36	127.5	3.2	1639	14	US-10-087-464-10	Sequence 10, Appl
37	126	3.2	699	15	US-10-282-122A-61334	Sequence 61334, A
38	126	3.2	961	16	US-10-767-701-47381	Sequence 47381, A
39	124	3.1	968	15	US-10-424-599-239683	Sequence 239683,
40	123	3.1	762	15	US-10-402-466A-20	Sequence 20, Appl
41	123	3.1	1019	16	US-10-408-765A-1661	Sequence 1661, Ap
42	122	3.1	965	14	US-10-150-559-2	Sequence 2, Appli
43	122	3.1	965	15	US-10-440-352-2	Sequence 2, Appli
44	122	3.1	972	15	US-10-282-122A-53353	Sequence 53353, A
45	120.5	3.1	2165	10	US-09-923-070A-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1

US-10-022-366A-2

; Sequence 2, Application US/10022366A

; Publication No. US20040050316A1

; GENERAL INFORMATION:

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OM protein - protein search, using sw model

Run on: December 10, 2004, 16:42:30 ; Search time 43 Seconds
(without alignments)
1152.082 Million cell updates/sec

Title: US-10-022-366A-2
Perfect score: 3949
Sequence: 1 MPLFKLPAEGKELDDAMGSF.....RYETWCYELNLIAEGLKSTE 747

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1724	43.7	600	4	US-09-270-767-32913	Sequence 32913, A
2	1724	43.7	600	4	US-09-270-767-48130	Sequence 48130, A
3	1461	37.0	610	4	US-09-248-796A-17399	Sequence 17399, A
4	1454	36.8	810	4	US-09-538-092-596	Sequence 596, App
5	140	3.5	226	4	US-09-270-767-42982	Sequence 42982, A
6	136.5	3.5	966	4	US-09-606-312-2	Sequence 2, Appli
7	132.5	3.4	334	4	US-09-543-681A-4632	Sequence 4632, Ap
8	127.5	3.2	338	4	US-09-489-039A-9479	Sequence 9479, Ap
9	124.5	3.2	352	4	US-09-328-352-6481	Sequence 6481, Ap
10	123	3.1	338	4	US-09-489-039A-8357	Sequence 8357, Ap
11	122	3.1	412	4	US-09-328-352-4751	Sequence 4751, Ap
12	120.5	3.1	2165	1	US-08-514-975B-2	Sequence 2, Appli

Drosophila melanogaster

OM protein - protein search, using sw model

Run on: December 10, 2004, 16:42:31 ; Search time 40 Seconds
(without alignments)
1796.848 Million cell updates/sec

Title: US-10-022-366A-2
Perfect score: 3949
Sequence: 1 MPLFKLPAEGKELDDAMGSF.....RYETWCYELNLIAEGLKSTE 747

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3728	94.4	747	2	I39444 <i>human</i>	AMP deaminase (EC
2	3607	91.3	747	1	A27366 <i>rat</i>	AMP deaminase (EC
3	2407.5	61.0	776	2	S68146 <i>human splice variant</i>	AMP deaminase (EC
4	2406	60.9	774	2	S68147 "	AMP deaminase (EC
5	1888.5	47.8	760	2	A44313 "	AMP deaminase (EC
6	1727.5	43.7	865	2	T15771 <i>C.elegans</i>	hypothetical prote
7	1510	38.2	600	2	T01259	AMP deaminase homo
8	1470.5	37.2	846	2	T39261	amp deaminase - fi
9	1454	36.8	810	2	S49744	AMP deaminase (EC
10	1451	36.7	924	2	T50996	probable AMP deami
11	1390.5	35.2	605	2	S59996	AMP deaminase (EC
12	671	17.0	797	2	S44546	probable membrane
13	656.5	16.6	888	2	S50801	AMP deaminase homo
14	409.5	10.4	88	2	S50184	AMP deaminase (EC

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OM protein - protein search, using sw model

Run on: December 10, 2004, 16:42:31 ; Search time 143 Seconds
(without alignments)
3005.628 Million cell updates/sec

Title: US-10-022-366A-2
Perfect score: 3949
Sequence: 1 MPLFKLPAEGKELDDAMGSF.....RYETWCYELNLIAEGLKSTE 747

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3728	94.4	747	1 AMD1_HUMAN	P23109 homo sapien
2	3607	91.3	747	1 AMD1_RAT	P10759 rattus norv
3	2788.5	70.6	717	2 Q6P3G5	Q6p3g5 brachydanio
4	2788.5	70.6	717	2 AAH63996	Aah63996 brachydan
5	2499	63.3	779	2 Q803X5	Q803x5 brachydanio
6	2422.5	61.3	766	2 Q8CFR4	Q8cfr4 mus musculu
7	2422.5	61.3	766	2 AAH56380	Aah56380 mus muscu
8	2412.5	61.1	766	1 AMD3_MOUSE	O08739 mus musculu
9	2406	60.9	767	1 AMD3_HUMAN	Q01432 homo sapien
10	2401	60.8	765	1 AMD3_RAT	O09178 rattus norv
11	1969	49.9	481	2 Q922J7	Q922j7 mus musculu
12	1890.5	47.9	798	2 Q9DBT5	Q9dbt5 mus musculu
13	1888.5	47.8	879	1 AMD2_HUMAN	Q01433 homo sapien
14	1830.5	46.4	860	2 Q7QFN2	Q7qfn2 anopheles g
15	1824.5	46.2	774	2 Q9VY76	Q9vy76 drosophila
16	1824.5	46.2	774	2 AAF48329	Aaf48329 drosophil